



Conseiller.ST25  
SUBSTITUTE SEQUENCE LISTING

<110> Conseiller, Emmanuel  
Debussche, Laurent  
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5'-1(p53)

<400> 1

agatctgtat ggaggagccg cag

23

<210> 2

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' -393 (p53)

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<400> 2  
agatctcatc agtctgagtc aggcccttc

29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide H175 3'

<400> 3  
ggggcagtgc ctcac

15

<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide w248 3'

<400> 4  
gggcctccag ttcac

15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide H273 3'

<400> 5  
acaaacatgc acctc

15

<210> 6

<211> 15

<212> DNA

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<213> Artificial Sequence

<220>

<223> oligonucleotide G281 3'

<400> 6

gcgccggcct ctccc

15

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5'-73

<400> 7

agatctgtgt ggcccctgca cca

23

<210> 8

<211> 1021

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 8

tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac  
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

48

ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

96

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

144

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca  
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

192

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt  
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys

240

65	Conseiller.ST25										80														
	70	75																							
aac Asn	cag Gln	ggc Gly	tat Tyr	gag Glu 85	ctg Leu	cac His	cgg Arg	gat Asp	ggc Gly 90	ttc Phe	tcc Ser	tgc Cys	agc Ser 95	gat Asp	atc Ile	288									
gat Asp	gag Glu	tgc Cys	ggc Gly 100	tac Tyr	tcc Ser	agt Ser	tac Tyr	ctc Leu 105	tgc Cys	cag Gln	tac Tyr	cgc Arg	tgt Cys 110	gtc Val	aac Asn	336									
gag Glu	cca Pro	ggc Gly 115	cga Arg	ttc Phe	tcc Ser	tgt Cys	cac His 120	tgc Cys	cca Pro	caa Gln	ggc Gly 125	tac Tyr 125	cag Gln	ctg Leu	ctg Leu	384									
gct Ala 130	aca Thr	agg Arg	ctc Leu	tgc Cys	caa Gln	gat Asp 135	att Ile	gac Asp	gag Glu	tgt Cys	gaa Glu 140	aca Thr	ggt Gly	gca Ala	cac His	432									
caa Gln 145	tgt Cys	tct Ser	gag Glu	gcc Ala	caa Gln 150	acc Thr	tgt Cys	gtc Val	aac Asn	ttc Phe 155	cat His	ggg Gly	ggt Gly	tac Tyr	cgc Arg 160	480									
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tca Ser	tcc Ser	att Ile 195	gtg Val	cac His	cgc Arg	tac Tyr	atg Met 200	agc Ser	atc Ile	acc Thr	tca Ser	gag Glu 205	cga Arg	agt Ser	gtg Val	624									
cct Pro 210	gct Ala	gac Asp	gtg Val	ttt Phe	cag Gln	atc Ile 215	cag Gln	gca Ala	acc Thr	tct Ser	gtc Val 220	tac Tyr	cct Pro	ggt Gly	gcc Ala	672									
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att Ile	agg Arg	caa Gln	atc Ile	aac Asn 245	aat Asn	gtc Val	agc Ser	gcc Ala	atg Met 250	ctg Leu	gtc Val	ctc Leu	gcc Ala	agg Arg 255	cca Pro	768									
gtg Val	acg Thr	gga Gly	ccc Pro 260	cgg Arg	gag Glu	tac Tyr	gtg Val	ctg Leu 265	gac Asp	ctg Leu	gag Glu	atg Met	gtc Val 270	acc Thr	atg Met	816									
aat Asn	tcc Ser	ctt Leu 275	atg Met	agc Ser	tac Tyr	cgg Arg	gcc Ala 280	agc Ser	tct Ser	gta Val	ctg Leu	aga Arg	ctc Leu	acg Thr	gtc Val	864									
ttt Phe 290	gtg Val	gga Gly	gcc Ala	tat Tyr	acc Thr	ttc Phe 295	tgaagaccct caggggaaggg ccatgtgggg									915									
gccccttccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt																975									
aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa																1021									

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<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<400> 9

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

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Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
275 280 285

Phe Val Gly Ala Tyr Thr Phe  
290 295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide c-myc 5'

<400> 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide c-myc 3'

<400> 11

gatctcaggt cctcctcgga gatacagcttc tgctccatg

39

<210> 12

# Conseiller.ST25

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' MCS oligonucleotide

<400> 12

gatctcgggc gacctgcatg caattcccgg gtgcggccgc gagct

45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' MCS oligonucleotide

<400> 13

cgcggccgca cccgggaatt gcatgcaggt cgaccga

37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' mMBP1

<400> 14

cggtactggc agaggtaact gg

22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<220>

<221> CDS

<222> (49)..(1377)

# Conseiller.ST25

<400> 15

gctgtggcag aaacccctga cttctgcca ccacctcca gcctcagg atg ctc cct 57  
Met Leu Pro  
1

ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg 105  
Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu  
5 10 15

ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc 153  
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser  
20 25 30 35

tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac 201  
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His  
40 45 50

tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt 249  
Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly  
55 60 65

gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc 297  
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg  
70 75 80

tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca 345  
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro  
85 90 95

gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct 393  
Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro  
100 105 110 115

gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg 441  
Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu  
120 125 130

cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac 489  
His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr  
135 140 145

cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg 537  
Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val  
150 155 160

gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac 585  
Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn  
165 170 175

ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga 633  
Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly  
180 185 190 195

cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc 681  
Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala  
200 205 210

cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc 729  
Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg  
215 220 225



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tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp	777
230 235 240	
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val	825
245 250 255	
aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu	873
260 265 270 275	
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala	921
280 285 290	
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr	969
295 300 305	
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser	1017
310 315 320	
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln	1065
325 330 335	
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser	1113
340 345 350 355	
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly	1161
360 365 370	
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe	1209
375 380 385	
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg	1257
390 395 400	
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr	1305
405 410 415	
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr	1353
420 425 430 435	
gtc ttt gtg gga gcc tat acc ttc tgaagaccct caggggaaggg ccatgtgggg Val Phe Val Gly Ala Tyr Thr Phe	1407
440	
gcccccttccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt	1467
aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa	1513

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<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly  
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

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Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
275 280 285

Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val  
305 310 315 320

Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser  
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln  
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
435 440

<210> 17

# Conseiller.ST25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' hMBP1

<400> 17

ctccgctccg aggtgatggt c

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5' hMBP1

<400> 18

tgtagctact ccagctacct c

21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 19

aagccagccg agccgccaga gccgcggggc gcgggggtgt cgcggggcca accccaggat 60

gctcccctgc gcctcctgcc taccggggtc tctactgctc tgggcgctgc tactgttgct 120

cttgggatca gcttctctc aggattctga agagcccgac agctacacgg aatgcacaga 180

tggctatgag tgggacccag acagccagca ctgccgggat gtcaacgagt gtctgaccat 240

ccctgaggcc tgcaaggggg aaatgaagtg catcaaccac tacgggggct acttgtgcct 300

gccccgctcc gctgccgtca tcaacgacct acacggcgag ggacccccgc caccagtgcc 360

tcccgtcaa caccccaacc cctgcccacc aggctatgag cccgacgatc aggacagctg 420

tgtggatgtg gacgagtgtg cccaggccct gcacgactgt cgccccagcc aggactgcc 480

taacttgcct ggctcctatc agtgcacctg ccctgatggt taccgcaaga tcgggcccga 540

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gtgtgtggac atagacgagt gccgctaccg ctactgccag caccgctgcg tgaacctgcc	600
tggctccttc cgctgccagt gcgagccggg cttccagctg gggcctaaca accgctcctg	660
tgttgatgtg aacgagtgtg acatgggggc cccatgcbag cagcgtgct tcaactccta	720
tgggaccttc ctgtgtcgct gccaccaggg ctatgagctg catcgggatg gcttctcctg	780
cagtgatatt gatgagtgtg gctactccag ctacctctgt cagtaccgct gcgtcaacga	840
gccaggccgt ttctcctgcc actgcccaca gggttaccag ctgctggcca cacgcctctg	900
ccaagacatt gatgagtgtg agtctggtgc gcaccagtgc tccgaggccc aaacctgtgt	960
caacttccat gggggctacc gctgcgtgga caccaaccgc tgcgtggagc cctacatcca	1020
ggctcttgag aaccgctgtc tctgcccggc ctccaaccct ctatgtcgag agcagccttc	1080
atccattgtg caccgctaca tgaccatcac ctcgagcgg ag	1122

<210> 20

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 20

tgtagctact ccagctacct ctgtcagtag cgctgcgtca acgagccagg ccgtttctcc	60
tgccactgcc cacaggggta ccagctgctg gccacacgcc tctgccaaga cattgatgag	120
tgtgagtctg gtgcgcacca gtgtccgag gcccaaacct gtgtcaactt ccatgggggc	180
taccgctgcb tggacaccaa ccgctgcgtg gagccctaca tccaggtctc tgagaaccgc	240
tgtctctgcc cggcctccaa cctctatgt cgagagcagc cttcatccat tgtgcaccgc	300
tacatgacca tcacctcgga gcgagcgtg cccgctgacg tgttccagat ccaggcgacc	360
tccgtctacc ccggtgccta caatgccttt cagatccgtg ctggaaactc gcagggggac	420
ttttacatta ggcaaatcaa caacgtcagc gccatgctgg tcctcgcccg gccggtgacg	480
ggcccccgga agtacgtgct ggacctggag atgggtacca tgaattccct catgagctac	540
cgggcccagct ctgtactgag gctcaccgtc tttgtagggg cctacacctt ctgaggagca	600
ggagggagcc accctccctg cagctaccct agctgaggag cctgttgtga ggggcagaat	660
gagaaaggca ataaaggag aaag	684

<210> 21

<211> 1480

# Conseiller.ST25

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21

aagccagccg agccgccaga gccgcggggcc gcgggggtgt cgcgggccca accccagg 58

atg ctc ccc tgc gcc tcc tgc cta ccc ggg tct cta ctg ctc tgg gcg 106  
Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag 154  
Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30

ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac 202  
Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45

agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc 250  
Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc 298  
Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc 346  
Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95

ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca gcc 394  
Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110

tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc 442  
Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125

cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct 490  
Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc 538  
Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc 586  
Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc 634  
Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac 682

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Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp	
		195					200					205				
atg	ggg	gcc	cca	tgc	gag	cag	cgc	tgc	ttc	aac	tcc	tat	ggg	acc	ttc	730
Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe	
	210					215					220					
ctg	tgt	cgc	tgc	cac	cag	ggc	tat	gag	ctg	cat	cgg	gat	ggc	ttc	tcc	778
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	
225					230					235					240	
tgc	agt	gat	att	gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac	826
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	
				245					250					255		
cgc	tgc	gtc	aac	gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggc	874
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	
			260					265					270			
tac	cag	ctg	ctg	gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	922
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	
	275						280					285				
tct	ggc	gcg	cac	cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	970
Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	
	290					295					300					
ggg	ggc	tac	cgc	tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	1018
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	
305					310					315					320	
cag	gtc	tct	gag	aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	1066
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	
				325					330					335		
cga	gag	cag	cct	tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	1114
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	
			340					345					350			
gag	cgg	agc	gtg	ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	1162
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	
		355					360					365				
tac	ccc	ggc	gcc	tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	1210
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	
	370					375					380					
ggg	gac	ttt	tac	att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	1258
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	
385					390					395				400		
ctc	gcc	cgg	ccg	gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	1306
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	
				405					410					415		
atg	gtc	acc	atg	aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	1354
Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	
			420					425					430			
agg	ctc	acc	gtc	ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca				1407
Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe						
		435				440										

Conseiller.ST25

ccctccctgc agctacccta gctgaggagc ctgttgtag gggcagaatg agaaaggcaa 1467  
taaagggaga aag 1480

<210> 22

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<400> 22

Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175



Conseiller.ST25

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile  
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser  
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln  
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
420 425 430

Conseiller.ST25

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 cDNA (partial sequence)

<400> 23

gctgtggcag aaacccctga cttctgcca ccacctcca gcctcaggat gctccctttt	60
gcctcctgcc tccccgggtc tttgctgctc tgggcgtttc tgctgttgct cttgggagca	120
gcgtccccac aggatcccgga ggagccggac agctacacgg aatgcacaga tggctatgag	180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct	240
tgcaaggggtg agatgaaatg catcaaccac tacggggggtt atttgtgtct gcctcgctct	300
gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa	360
caaccaaacc cttgcccga gggctacgag cctgatgaac aggagagctg tgtggatgtg	420
gacgagtgtg cccaggcttt gcatgactgt cgccctagtc aggactgcca taaccttcct	480
ggctcctacc agtgcacctg ccctgatggt taccgaaaaa ttggaccgga atgtgtggac	540
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggctctttt	600
cgatgccagt gtgagccagg cttccagttg ggacctaa accgctcttg tgtggatgtg	660
aatgagtgtg acatgggagc cccatgtgag cagcgtgct tcaactccta tgggaccttc	720
ctgtgtcgct gtaaccaggg ctatgagctg caccgggatg gcttctcctg cagcgatatc	780
gatgagtgcg gctactccag ttacctctgc cagtacc	817

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-GAPDH oligonucleotide

<400> 24

cggagtcaac ggatttggtc gtat

24

# Conseiller.ST25

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atggtggtga agac

24

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-beta-actin oligonucleotide

<400> 26

cggttggcct tggggttcag ggggg

25

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-MBP1 oligonucleotide

<400> 27

gccctgatgg ttaccgcaag a

21

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense MBP1 oligonucleotide

# Conseiller.ST25

<400> 28  
agcccccatg gaagttgaca c 21

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-beta-actin oligonucleotide

<400> 29  
gtggggcgcc ccaggcacca 20

<210> 30

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 30  
tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac 48  
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg 96  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct 144  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca 192  
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc 240  
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att 288  
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac 336

Conseiller.ST25

Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg	Cys	Val	Asn								
			100					105					110										
gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggg	tac	cag	ctg	ctg	384							
Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr	Gln	Leu	Leu								
		115					120					125											
gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	tct	ggg	gcg	cac	432							
Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	Ser	Gly	Ala	His								
	130					135					140												
cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	ggg	ggc	tac	cgc	480							
Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	Gly	Gly	Tyr	Arg								
	145				150					155					160								
tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	cag	gtc	tct	gag	528							
Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	Gln	Val	Ser	Glu								
				165					170					175									
aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	cga	gag	cag	cct	576							
Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Glu	Gln	Pro								
			180					185					190										
tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	gag	cgg	agc	gtg	624							
Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu	Arg	Ser	Val								
		195					200					205											
ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	tac	ccc	ggg	gcc	672							
Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly	Ala								
	210					215					220												
tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	ggg	gac	ttt	tac	720							
Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	Gly	Asp	Phe	Tyr								
	225				230					235					240								
att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	ctc	gcc	cgg	ccg	768							
Ile	Arg	Gln	Ile	Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg	Pro									
				245				250					255										
gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	atg	gtc	acc	atg	816							
Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met	Val	Thr	Met								
			260					265					270										
aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	agg	ctc	acc	gtc	864							
Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg	Leu	Thr	Val								
		275					280					285											
ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag gagggagcca ccctccctgc									915							
Phe	Val	Gly	Ala	Tyr	Thr	Phe																	
	290					295																	
agctacccta gctgaggagc ctgttgtag gggcagaatg agaaaggcaa taaagggaga															975								
aagaaagtcc tggtggctga ggtgggcggg tcacactgca ggaagcctca ggctggggca															1035								
gggtggcact tggggggggca ggccaagtgc acctaaatgg gggctctctat atgttcaggc															1095								
ccagggggccc ccattgacag gagctgggag ctctgcacca cgagcttcag tcaccccgag															1155								
aggagaggag gtaacgagga gggcggactc caggccccgg ccagagatt tggacttggc															1215								
tggcttgacag ggggtcctaag aaactccact ctggacagcg ccaggaggcc ctgggttcca															1275								

Conseiller.ST25

ttcctaactc tgcctcaaac tgtacatttg gataagccct agtagttccc tgggcctgtt 1335  
 tttctataaa acgaggcaac tgg 1358

<210> 31

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<400> 31

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
 1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
 20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
 130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
 145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu  
 165 170 175

# Conseiller.ST25

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr  
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
275 280 285

Phe Val Gly Ala Tyr Thr Phe  
290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>

<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

<400> 32

gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat	48
Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His	
1 5 10 15	

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc	96
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg	
20 25 30	

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc	144
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys	
35 40 45	

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac	192
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Conseiller.ST25																
Ile	Asp	Val	Asn	Glu	Cys	Trp	Val	Ser	Pro	Gly	Arg	Leu	Cys	Gln	His	
50						55					60					
aca	tgt	gag	aac	aca	ccg	ggc	tcc	tac	cgc	tgc	tcc	tgc	gct	gct	ggc	240
Thr	Cys	Glu	Asn	Thr	Pro	Gly	Ser	Tyr	Arg	Cys	Ser	Cys	Ala	Ala	Gly	
65					70				75						80	
ttc	ctt	ttg	gcc	gca	gat	ggc	aaa	cat	tgt	gaa	gat	gtg	aac	gag	tgc	288
Phe	Leu	Leu	Ala	Ala	Asp	Gly	Lys	His	Cys	Glu	Asp	Val	Asn	Glu	Cys	
				85					90					95		
gag	act	cgg	cgc	tgc	agc	cag	gaa	tgt	gcc	aac	atc	tat	ggc	tcc	tat	336
Glu	Thr	Arg	Arg	Cys	Ser	Gln	Glu	Cys	Ala	Asn	Ile	Tyr	Gly	Ser	Tyr	
			100					105					110			
cag	tgc	tac	tgc	cgt	cag	ggc	tac	cag	ctg	gca	gag	gat	ggg	cat	acc	384
Gln	Cys	Tyr	Cys	Arg	Gln	Gly	Tyr	Gln	Leu	Ala	Glu	Asp	Gly	His	Thr	
		115					120					125				
tgc	aca	gac	atc	gat	gag	tgt	gca	cag	ggc	gcg	ggc	att	ctc	tgt	acc	432
Cys	Thr	Asp	Ile	Asp	Glu	Cys	Ala	Gln	Gly	Ala	Gly	Ile	Leu	Cys	Thr	
	130					135					140					
ttc	cgc	tgt	gtc	aac	gtg	cct	ggg	agc	tac	cag	tgt	gca	tgc	cca	gag	480
Phe	Arg	Cys	Val	Asn	Val	Pro	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Pro	Glu	
145					150					155					160	
caa	ggg	tat	aca	atg	atg	gcc	aac	ggg	agg	tcc	tgc	aag	gac	ctg	gat	528
Gln	Gly	Tyr	Thr	Met	Met	Ala	Asn	Gly	Arg	Ser	Cys	Lys	Asp	Leu	Asp	
				165					170					175		
gag	tgt	gca	ctg	ggc	acc	cac	aac	tgc	tct	gag	gct	gag	acc	tgc	cac	576
Glu	Cys	Ala	Leu	Gly	Thr	His	Asn	Cys	Ser	Glu	Ala	Glu	Thr	Cys	His	
			180					185					190			
aat	atc	cag	ggg	agt	ttc	cgc	tgc	ctg	cgc	ttt	gat	tgt	cca	ccc	aac	624
Asn	Ile	Gln	Gly	Ser	Phe	Arg	Cys	Leu	Arg	Phe	Asp	Cys	Pro	Pro	Asn	
		195					200					205				
tat	gtc	cgt	gtc	tca	caa	acg	aag	tgc	gag	cgc	acc	aca	tgc	cag	gat	672
Tyr	Val	Arg	Val	Ser	Gln	Thr	Lys	Cys	Glu	Arg	Thr	Thr	Cys	Gln	Asp	
	210					215					220					
atc	acg	gaa	tgt	caa	acc	tca	cca	gct	cgc	atc	acg	cac	tac	cag	ctc	720
Ile	Thr	Glu	Cys	Gln	Thr	Ser	Pro	Ala	Arg	Ile	Thr	His	Tyr	Gln	Leu	
225					230				235						240	
aat	ttc	cag	aca	ggc	cta	ctg	gta	cct	gca	cat	atc	ttc	cgc	atc	ggc	768
Asn	Phe	Gln	Thr	Gly	Leu	Leu	Val	Pro	Ala	His	Ile	Phe	Arg	Ile	Gly	
				245					250					255		
cct	gct	ccc	gcc	ttt	gct	ggg	gac	acc	atc	tcc	ctg	acc	atc	acg	aag	816
Pro	Ala	Pro	Ala	Phe	Ala	Gly	Asp	Thr	Ile	Ser	Leu	Thr	Ile	Thr	Lys	
			260					265					270			
ggc	aat	gag	gag	ggc	tac	ttc	gtc	aca	cgc	aga	ctc	aat	gcc	tac	act	864
Gly	Asn	Glu	Glu	Gly	Tyr	Phe	Val	Thr	Arg	Arg	Leu	Asn	Ala	Tyr	Thr	
		275					280					285				
ggt	gtg	gta	tcc	ctg	cag	cgg	tct	gtt	ctg	gag	ccg	cgg	gac	ttt	gcc	912
Gly	Val	Val	Ser	Leu	Gln	Arg	Ser	Val	Leu	Glu	Pro	Arg	Asp	Phe	Ala	
	290					295					300					



# Conseiller.ST25

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960  
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
 305 310 315 320

ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgagggtgaca 1009  
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
 325 330

tgtcaggcaa tccctccagg tgatgcctgg gcggtgggca gctgcgccac tcctaagtgg 1069

ctttttgctg tgactctgta acttaactta atcatgctga gctgggttggc cttgagtctc 1129

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<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine fibulin 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
 1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
 20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
 35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His  
 50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly  
 65 70 75 80

# Conseiller.ST25

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys  
 85 90 95  
 Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr  
 100 105 110  
 Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr  
 115 120 125  
 Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr  
 130 135 140  
 Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu  
 145 150 155 160  
 Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp  
 165 170 175  
 Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His  
 180 185 190  
 Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn  
 195 200 205  
 Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp  
 210 215 220  
 Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu  
 225 230 235 240  
 Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly  
 245 250 255  
 Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys  
 260 265 270  
 Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr  
 275 280 285  
 Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
 290 295 300  
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
 305 310 315 320  
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro

325

Conseiller.ST25  
330

<210> 34

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine N-terminal signal sequence

<400> 34

Ala Val Ala Glu Thr Pro Asp Phe Cys Pro Pro Pro Ser Leu Arg  
1 5 10 15

<210> 35

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Human N-terminal signal sequence

<400> 35

Ser Gln Pro Ser Arg Gln Ser Arg Gly Pro Arg Gly Cys Arg Gly Pro  
1 5 10 15

Asn Pro Arg